STIC Biotechnology Systems Branch

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CRF Problem Report

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: _10/593,426_
Filing Date: _9/19/06_
Date Processed by STIC: _9/27/06_

STIC Contact: **Mark Spencer: Telephone: 571-272-2510; Fax: 571-273-0221**

Nature of CRF Problem:

_____ (circle one) Damaged or Unreadable (for Unreadable, see attached)
_____ Blank (no files on CRF) (see attached)
_____ Empty file (filename present, but no bytes in file) (see attached)
_____ Wrong file saved to CRF (invention title, docket number, or applicant(s) do not match those in official application) (see attached)
_____ Not saved in ASCII text
_____ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should only be the Sequence Listing.
_____ Did not contain a Sequence Listing. (see attached sample)
__✓__ Other: _Alpha Numeric headings in Sequence._

PLEASE USE THE CHECKER VERSION 4.3.1 PROGRAM TO REDUCE ERRORS. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 08/30/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER $10/593,426$

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length — Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences (NEW RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ✓ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220> — Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

(handwritten top:) 10/593,426
(handwritten:) (Sample of submitted file)   PAGE 1

SEQUENCE LISTING
<110> PAPES, Fabio
       GERHARDT, Isabel Rodrigues
       ARRUDA, Paulo

<120> CAMBIUM/XYLEM-PREFERRED PROMOTERS AND USES THEREOF

<130> ALEL 202.1 PCT   *(handwritten:)* pls insert prior Application Number and date,

<140>   *(handwritten:)* pls insert prior Application Number and date,
<141>

<150> US 60/560,227
<151> 2004-04-06

<160> 41

<170> PatentIn version 3.2   *(handwritten:)* pls delete, invalid numeric identifier.

(handwritten right margin:) These types of errors are seen globally throughout the sequence.

<200> SEQUENCE CHARACTERISTICS:
<210> SEQ ID NO 1
<211> LENGTH: 3035
<212> TYPE: DNA
<213> ORGANISM: Populus sp.   *(handwritten:)* pls do Not insert Alpha Numeric headings in sequence,
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)...(3035)
<223> OTHER INFORMATION: Sucrose synthase (SUSY) promoter
<400> SEQUENCE: 1

(handwritten left margin:) pls delete

```
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   140
tctatttatt ttgatatatt acatcaagaa taaatttaa aaaaataatt tttaaaattt acttaaccac
   210
gcaatacata aaaaataata gaacccacca acctaagaat acttgtcaat gcatagaagt acacctgcta
   280
gttcttaaaa ccaacaaaag gaagcaaagt agatctctga gtcaaaaacc agaggaaacc atagaaacac
   350
aaataataa taataataat aataataata aaattaattt aacttggtgt aataataaaa ttaatttaat
   420
cacaaagagt gtaactcaac tagtcatgtt ctaaatttat tctctagaga ttactagttt gagttttaca
   490
aattttaagg ccactgaaga tttatatagt cattaatttc agaatatata agattagttg agttacgtat
   560
aacttgatta aaaaatcata ttaataaaaa taaaaaaatt aatttaaagg tttaagaaat caaattaaga
   630
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   980
```

(handwritten bottom:) pls see item #1 on error Summary sheet.

```
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1680
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1750
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1820
cgatgccgta taaataatat taatatcttt gaatcagtat gtatattaat taaaattaat tttttttcaaa
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1960
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2660
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2730
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2800
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2940
ccctacaaat aatattgagt tgttgctggt cttaattcct attatctgtt attactccca ctgattgctt
```

(handwritten annotations in right margin:)

SAme errors

See
item
1
on error
Summary
Sheet?

```
3010
tctgtttctc ttaaggagct atggc
3035
```

← Same error

```
<200> SEQUENCE CHARACTERISTICS:
<210> SEQ ID NO 13
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM/SOURCE  synthetic
<221> NAME/KEY  primer/oligonucleotide
<400> SEQUENCE: 13
5- GCCATAGCTC CTTAAGAGAA ACAGAAAGCA A -3
```

pls delete, Invalid numeric identifier

Invalid response — insert on line <223>

delete

pls use lower case

delete

See item # 10 on error summary sheet.

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

FYI:

<213> responses CAN ONLY be either Artificial/ Unknown or genus/species,